

## Appendix A (selected from SCORE)

Result 1: SEQ ID No: 8 w/ Asp @ position #3.

RESULT 2 from  
ABM91587

ID ABM91587 standard; protein; 866 AA.  
XX  
AC ABM91587;  
XX  
DT 02-JUN-2005 (first entry)  
XX  
DE M. xanthus protein sequence, seq id 10786.  
XX  
KW Transgenic plant; DNA replication; gene regulation; gene  
expression.  
XX  
OS Myxococcus xanthus.  
XX  
PN US6833447-B1.  
XX  
PD 21-DEC-2004.  
XX  
PF 10-JUL-2001; 2001US-00902540.  
XX  
PR 10 JUL-2000; 2000US-0217883P.  
XX  
PA (MONS ) MONSANTO TECHNOLOGY LLC.  
XX  
PI Goldman BS, Hinkle GJ, Slater SC, Wiegand RC;  
XX  
DR WPI; 2005-028716/03.  
XX  
PT New substantially purified Myxococcus xanthus nucleic acid  
molecule  
PT encoding a nitrite reductase, useful for determining gene  
expression,  
PT identifying mutations in a gene of interest, and for constructing  
PT mutations in a gene of interest.  
XX  
PS Example 2; SEQ ID NO 10786; 25pp; English.  
XX  
CC The invention relates to a substantially purified nucleic acid  
molecule  
CC encoding a nitrite reductase of SEQ ID NO. 11926. Further  
disclosed is a  
CC recombinant DNA construct for expression of a nitrite reductase  
gene in a  
CC plant cell, and a plant cell comprising the recombinant DNA  
construct.  
CC The nucleic acid is useful for determining gene expression,  
identifying  
CC mutations in a gene of interest, and for constructing mutations in  
a gene  
CC of interest. Sequences given in records for SEQ IDs 9692 16825  
represent

CC a group of 7134 *Mxyococcus xanthus* proteins and peptides. Note:  
 The  
 CC sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from  
 USPTO  
 XX  
 SQ Sequence 866 AA;

Query Match 100.0%; Score 35; DB 9; Length 866;  
 Best Local Similarity 100.0%; Pred. No. 9.7e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0;  
 Gaps 0;

QY	1 DVDAWL 6	1 DVDAWL 866
DB	843 DVDAWL 848	843 DVDAWL 851

Result 2: SEQ ID No: 8 w/ Glu @ position #3.

RESULT 11  
 ABO73966  
 ID ABO73966 standard; protein; 274 AA.  
 XX  
 AC ABO73966;  
 XX  
 DT 29-JUL-2004 (first entry)  
 XX  
 DE *Pseudomonas aeruginosa* polypeptide #6141.  
 XX  
 KW Bacterial infection; *Pseudomonas aeruginosa* infection;  
 antibacterial.  
 XX  
 OS *Pseudomonas aeruginosa*.  
 XX  
 PN US6551795-B1.  
 XX  
 PD 22-APR-2003.  
 XX  
 PF 18-FEB-1999; 99US-00252991.  
 XX  
 PR 18-FEB-1998; 98US 0074788P.  
 PR 27-JUL 1998; 98US-0094190P.  
 XX  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 XX  
 PI Rubenfield MJ, Nolling J, Deloughery C, Bush D;  
 XX  
 DR WPI; 2003-615309/58.  
 DR N-PSDB; ABD07537.  
 XX  
 PT Novel isolated nucleic acid encoding *Pseudomonas aeruginosa*  
 polypeptide,  
 PT useful as molecular targets for diagnostics, prophylaxis and  
 treatment of

PT pathological conditions resulting from bacterial infection.  
 XX  
 PS Disclosure; SEQ ID NO 22712; 455pp; English.  
 XX  
 CC The invention relates to *Pseudomonas aeruginosa* polypeptides and the  
 CC polynucleotides encoding them. The sequences are useful in  
 CC diagnosis and  
 CC therapy of pathological conditions, as molecular targets for  
 CC diagnostics,  
 CC prophylaxis and treatment of pathological conditions resulting  
 CC from a  
 CC bacterial infection, for evaluating a compound, such as a  
 CC polypeptide,  
 CC for the ability to bind a *P. aeruginosa* nucleic acid, as  
 CC components of  
 CC effective antibacterial targets, as targets for antibacterial  
 CC drugs,  
 CC including anti-*P. aeruginosa* drugs, as templates for recombinant  
 CC production of *P. aeruginosa*-derived peptides or polypeptides, as  
 CC target  
 CC components for diagnosis and/or treatment of *P. aeruginosa*-caused  
 CC infection, and in detection of *P. aeruginosa* sequences or other  
 CC sequences  
 CC of *Pseudomonas* species using biochip technology. Sequences  
 AB067826-  
 CC AB084396 represent *P. aeruginosa* polypeptides of the invention.  
 Note: The  
 CC sequence data for this patent did not form part of the printed  
 CC specification but was obtained in electronic format from USPTO at  
 CC seqdata.uspto.gov/sequence.html  
 XX  
 SQ Sequence 274 AA;

Query Match 100.0%; Score 34; DB 7; Length 274;  
 Best Local Similarity 100.0%; Pred. No. 3.6e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0;  
 Caps 0;

OY 1 DVEAWL 6 ~ DVXAWLXXR 9  
 Db 180 DVEAWL 185 180 DVEAWLQLF 188

Result 3: SEQ ID No: 8 w/ Gly @ position #3.

RESULT 9  
 ASNT\_BACSU  
 ID ASNH\_BACSU STANDARD; PRT; 747 AA.  
 AC P42113;  
 DT 01-NOV-1995, integrated into UniProtKB/Swiss-Prot.  
 DT 01-NOV-1995, sequence version 1.  
 DT 13-JUN-2006, entry version 48.  
 DE Asparagine synthetase [glutamine-hydrolyzing] 2 (EC 6.3.5.4).

(0)

GN Name=asnH; OrderedLocusNames=BSU39920; ORFNames=S14NR, VE7AR;  
OS Bacillus subtilis.  
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
OX NCBI\_TaxID=1423;  
RN [1]  
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].  
RC STRAIN=168 / BGSC1A1;  
RX MEDLINE=96093926; PubMed=7584049; DOI=10.1093/dnareg/2.2.61;  
RA Yoshida K., Seki S., Fujimura M., Miwa Y., Fujita Y.;  
RT "Cloning and sequencing of a 36-kb region of the Bacillus subtilis  
RT genome between the gnt and iol operons.";  
RL DNA Res. 2:61-69(1995).  
RN [2]  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
RC STRAIN=168;  
RX MEDLINE=98044033; PubMed=9384377; DOI=10.1038/36786;  
RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,  
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,  
RA Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron  
S.,  
RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,  
RA Choi S.-K., Codani J.-J., Connerton I.F., Cummings N.J., Daniel  
R.A.,  
RA Denizot F., Devine K.M., Duesterhoeft A., Ehrlich S.D., Emmerson  
P.T.,  
RA Entian K. D., Errington J., Fabret C., Ferrari E., Foulger D.,  
RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,  
RA Chim S.-Y., Glaser P., Goffeau A., Golightly B.J., Grandi G.,  
RA Guiseppe G., Guy B.J., Haga K., Haiech J., Harwood C.R., Honaut  
A.,  
RA Hilbert H., Holsappel S., Hosono S., Hullo M.-F., Itaya M.,  
RA Jones L.-M., Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard  
M.,  
RA Klein C., Kobayashi Y., Koetter P., Koningstein G., Krogh S.,  
RA Kumano M., Kurita K., Lapidus A., Lardinois S., Lauber J.,  
RA Lazarevic V., Lee S.-M., Levine A., Liu H., Masuda S., Maubel C.,  
RA Medigue C., Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai  
S.,  
RA Noback M., Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B.,  
RA Park S.-H., Parro V., Pohl T.M., Portetelle D., Porwollik S.,  
RA Prescott A.M., Presecan E., Pujic P., Purnelle B., Rapoport G.,  
RA Rey M., Reynolds S., Rieger M., Rivolta C., Rocha E., Roche B.,  
RA Rose M., Sadaie Y., Sato T., Scanlan E., Schleich S., Schroeter  
R.,  
RA Scoffone F., Sekiguchi J., Sekowska A., Seror S.J., Serror P.,  
RA Shin B.-S., Soldo B., Sorokin A., Tacconi E., Takagi T., Takahashi  
H.,  
RA Takemaru K., Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P.,  
RA Tognoni A., Tosato V., Uchiyama S., Vandenbol M., Vannier F.,  
RA Vassarotti A., Viari A., Wambutt R., Wedler E., Wedler H.,  
RA Weitzenegger T., Winters P., Wipat A., Yamamoto H., Yamane K.,  
RA Yasumoto K., Yata K., Yoshida K., Yoshikawa H.-F., Zumstein E.,  
RA Yoshikawa H., Danchin A.;  
RT "The complete genome sequence of the Gram-positive bacterium  
Bacillus  
RT subtilis.";  
RL Nature 390:249-256(1997).

11

RN [3]  
 RP CHARACTERIZATION.  
 RX MEDLINE=99429856; PubMed=10498721;  
 RA Yoshida K., Fujita Y., Ehrlich S.D.;  
 RT "Three asparagine synthetase genes of *Bacillus subtilis*.";  
 RL J. Bacteriol. 181:6081-6091(1999).  
 CC -!- CATALYTIC ACTIVITY: ATP + L-aspartate + L-glutamine = AMP +  
 CC diphosphate + L-asparagine + L-glutamate.  
 CC -!- PATHWAY: Amino-acid biosynthesis; L-asparagine biosynthesis;  
 L-  
 CC asparagine from L-aspartate (L-glutamine route): single step  
 CC [final step].  
 CC -!- SIMILARITY: Belongs to the asparagine synthetase family.  
 CC -!- SIMILARITY: Contains 1 type-2 glutamine amidotransferase  
 domain.  
 CC -----

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 License  
 CC -----

DR EMBL; AB005554; BAA21593.1; -; Genomic\_DNA.  
 DR EMBL; Z99124; CAB16028.1; -; Genomic\_DNA.  
 OR PIR; A69591; A69591.  
 DR HSSP; P22106; 1CT9.  
 DR GenomeReviews; AL009126\_GR; BSU39920.  
 DR SubtiList; AG11116; asnH.  
 DR BioCyc; BSUB1423:BSU3988-MONOMER;  
 DR InterPro; IPR006426; Asn\_synth\_AKH.  
 DR InterPro; IPR001962; Asn\_synthase.  
 DR InterPro; IPR000583; GATase\_2.  
 DR Pfam; PF00733; Asn\_synthase; 1.  
 DR Pfam; PF00310; GATase\_2; 1.  
 DR TIGRFAMS; TIGR01536; asn\_synth\_AEB; 1.  
 KW Amino-acid biosynthesis; Asparagine biosynthesis; Complete  
 proteome;  
 KW Glutamine amidotransferase; Ligase.  
 FT CHAIN 1 747 Asparagine synthetase [glutamine-  
 FT hydrolyzing] 2.  
 FT /FTID=PRO\_0000056933.  
 FT REGION 1 175 Glutamine amidotransferase.  
 FT ACT\_SITE 2 2 For GATase activity (By similarity).  
 SQ SEQUENCE 747 AA; 85849 MW; 55447E3732806390 CRC64;

Query Match 100.0%; Score 35; DB 1; Length 747;  
 Best Local Similarity 100.0%; Pred. No. 5.5e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0;  
 Gaps 0;

Oy 1 DVGAWL 6 1 DVXFWLXXR 9  
 |||||  
 Db 690 DVGAWL 695 690 DVGAWLHIL 698

Result 4: SEQ ID No: 8 w/ Asp @ position #3.

RESULT 1

T43012

conserved hypothetical protein - fission yeast (Schizosaccharomyces pombe) (fragment)

C;Species: Schizosaccharomyces pombe

C;Date: 11-Jan-2000 #sequence\_revision 11-Jan-2000 #text\_change 09-Jul-2004

C;Accession: T43012

R;Yoshioka, S.; Kato, K.; Nakai, K.; Okayama, H.; Nojima, H.  
DNA Res. 4, 363-369, 1997

A;Title: Identification of open reading frames in Schizosaccharomyces pombe cDNAs.

A;Reference number: Z17323; MUID:98162722; PMID:9501991

A;Accession: T43012

A;Status: preliminary; translated from GB/EMBL/DDEJ

A;Molecule type: mRNA

A;Residues: 1 329

A;Cross-references: UNIPROT:Q9P7X4; UNIPARC:UP1000016910B; EMBL:D89208;  
NID:g1749623; PIDN:BAAL3869.1; PID:g1749624

A;Experimental source: strain PR745

Query Match 100.0%; Score 35; DB 2; Length 329;  
Best Local Similarity 100.0%; Pred. No. 27;  
Matches 6; Conservative 0; Mismatches 0; Indels 0;  
Gaps 0;

Oy 1 DVDWL 6  
      |||||  
Db 313 DVDWL 318

1 DVxAWLYVR 9  
313 DVDWLQSG 327